



OIKE

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RAW SEQUENCE LISTING

DATE: 03/14/2002

PATENT APPLICATION: US/10/087,667

TIME: 14:06:12

Input Set : A:\Uvm-0001.app

Output Set: N:\CRF3\03142002\J087667.raw

3 <110> APPLICANT: Bramley, John A.
 4 Plaut, Karen I.
 5 Kerr, David
 7 <120> TITLE OF INVENTION: TREATMENT OF STAPHYLOCOCCUS INFECTIONS
 9 <130> FILE REFERENCE: Mastitis
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/087,667
 12 <141> CURRENT FILING DATE: 2002-02-28
 14 <160> NUMBER OF SEQ ID NOS: 10
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1486
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Staphylococcus simulans
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 25 gattcatatt attttaacac aatcagtttag aatttcaaaa atcttaaagt caatttttga 120
 26 gtgtgtttgt atatttcac aaatcaatc aatattattt tactttcttc atcgtaaata 180
 27 aatgtaatat ttataaaaat atgctattct cataaatgta ataataaatt aggaggtatt 240
 28 aaggttgaag aaacaaaaa acaattatta tacgagacct ttagctattg gactgagtag 300
 29 atttgcccta gcatctattg tttatggagg gattcaaaat gaaacacatg cttctgaaaa 360
 30 aagtaatatg gatgtttcaa aaaaagtagc tgaagtagag acttcaaaaag cccagtaga 420
 31 aaatacagct gaagtagaga cttcaaaaagc tccagtagaa aatacagctg aagtagagac 480
 32 ttcaaaaagc ccagtagaaa atacagctga agtagagact tcaaaaagctc cagtagaaaa 540
 33 tacagctgaa gtagagactt caaaagctcc ggtagaaaat acagctgaag tagagacttc 600
 34 aaaagcccca gtagaaaata cagctgaagt agagacttca aaagccctgg ttcaaaatag 660
 35 aacagcttta agagctgcaa cacatgaaca ttacgacaa tgggtgaata attacaaaaa 720
 36 aggatattgg tacggtcctt atccattagg tataaatggc ggtatgcact acggagttga 780
 37 tttttttatg aatattggaa caccagtaaa agctatttca agcggaaaaa tagttgaagc 840
 38 tgggttgagt aattacggag gaggtaatca aataggctct attgaaaatg atggagtgc 900
 39 tagacaatgg tatatgcac taagtaaata gtaggagatt gtaggagatt atgtcaaagc 960
 40 tgggtcaaata atcggttggg ctggaagcac tggttattct acagcaccac atttacactt 1020
 41 ccaaagaatg gtttaattcat tttcaaattc aactgccccaa gatccaatgc ctttcttaaa 1080
 42 gaggcgagga tatggaaaag caggtggtac agtaactcca acgcccgaata caggttgga 1140
 43 aacaaacaaa tatggcacac tatataaatc agagtcagct agcttcacac ctaatacaga 1200
 44 tataataaca agaacgactg gtccatttag aagcatgccg cagtcaggag tcttaaaagc 1260
 45 aggtcaaaca attcattatg atgaagtgat gaaacaagac ggtcatgttt gggtaggtta 1320
 46 tacaggtaac agtggccaac gtatttactt gcctgtaaga acatggaata aatctactaa 1380
 47 tacttttaggt gttctttggg gaactataaa gtgagcgcgc tttttataaa cttatatgat 1440
 48 aattagagca aataaaaatt tttctcatt cctaaagttg aagctt 1486
 51 <210> SEQ ID NO: 2
 52 <211> LENGTH: 388
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Staphylococcus simulans

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56 <400> SEQUENCE: 2

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58   1      5      10      15
60 Leu Ser Thr Phe Ala Leu Ala Ser Ile Val Tyr Gly Gly Ile Gln Asn
61      20      25      30
63 Glu Thr His Ala Ser Glu Lys Ser Asn Met Asp Val Ser Lys Lys Val
64      35      40      45
66 Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val
67      50      55      60
69 Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser
70  65      70      75      80
72 Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro
73      85      90      95
75 Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn
76      100     105     110
78 Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu
79      115     120     125
81 Val Glu Thr Ser Lys Ala Leu Val Gln Asn Arg Thr Ala Leu Arg Ala
82      130     135     140
84 Ala Thr His Glu His Ser Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr
85 145     150     155     160
87 Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly
88      165     170     175
90 Val Asp Glu Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser
91      180     185     190
93 Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln
94      195     200     205
96 Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Glu Tyr Met His
97      210     215     220
99 Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln
100 225     230     235     240
102 Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu
103      245     250     255
105 His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp
106      260     265     270
108 Pro Met Pro Phe Leu Lys Ala Ser Gly Tyr Gly Lys Ala Gly Gly Thr
109      275     280     285
111 Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr
112      290     295     300
114 Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile
115 305     310     315     320
117 Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu
118      325     330     335
120 Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly
121      340     345     350
123 His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu
124      355     360     365
126 Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp
127      370     375     380

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129 Gly Thr Ile Lys

130 385

133 <210> SEQ ID NO: 3

134 <211> LENGTH: 741

135 <212> TYPE: DNA

136 <213> ORGANISM: Staphylococcus simulans

138 <400> SEQUENCE: 3

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141 attggaacac cagtaaaagc tatttcaagc ggaaaaatag ttgaagctgg ttggagtaat 180
142 tacggaggag gtaatcaaat aggtcttatt gaaaatgatg gagtgcatag acaatgggat 240
143 atgcatctaa gtaaatataa tgtaaagta ggagattatg tcaaagctgg tcaaataatc 300
144 ggttggtctg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatgggt 360
145 aactcatttt cacagtcaac tgcccaagat ccaatgcctt tcttaaagag cgcaggatat 420
146 ggaaaagcag gtgttacagt aactccaacg ccgaatacag gttggaaaac aaacaaatat 480
147 ggcacactat ataaatcaga gtacgctagc ttcacaccta atacagatat aataacaaga 540
148 acgactggtc catttagaag catgccgcag tcaggagtct taaaagcagg tcaacaatt 600
149 cattatgatg aagtgatgaa acaagacggg catgtttggg taggttatac aggtaacagt 660
150 ggccaacgta tttacttgcc tgtgagaaca tggcagaagt ctactaatac tctgggtgtt 720
151 ctgtggggaa ctataaagt a
152                                     741

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154 <210> SEQ ID NO: 4

155 <211> LENGTH: 1520

156 <212> TYPE: DNA

157 <213> ORGANISM: Staphylococcus simulans

159 <400> SEQUENCE: 4

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161 tcgcgcaccg tgtgaaccgc attgaggaat ggccgttcgg caagcgcatt tacggcctcg 120
162 atttgaacgt gcgtcgcacg acagcgtcgc gccgcgggtc agagtccggc gccgcgggta 180
163 tacggacagc gatcgcggcg tccgcgcgat acgaacgggc gtgcgcgtca gtcgcatgca 240
164 ccgctcgcgg ctggcggttc ggcttcgcgg gcgcgcgcgg gtccaccact cttcaaacgt 300
165 ctttctcggg agcagcatat gaagaagatt tccaaggcgg gactgggggt ggcgctgggt 360
166 tgcgcgctgg cgacgatcgg cggcaacgca gcgcgcaggg ccacggctca gcggcgagga 420
167 tctggtgtat tctacgacga gatgttcgac ttgcacatcg atgcgcatct ggccaagcat 480
168 gcgcgcgcatc tgcacaagca ctgcggaagag atctgcgact gggccgggta cagcgggatc 540
169 agccgaagtg ttgatcgcgc tgatggagca gcagagcgcg cggtcacgcc aagcgcgcga 600
170 cgaatcgtcc gttcggcaag ctggcgcgcg ccgacggctt cggcgcgcag accgcgagg 660
171 tcgcgctggc gctgcgcgag tcgctgtacg agcgcgatcc cgacgcgcca aggggcccgt 720
172 gacgctggcc cgcgccaatc cgctgcaggc gctgttcgag cgttcgggca acaacgagcc 780
173 ggcggccgcg ctgcgcggcg acggcgagtt ccagctgggt tacggccgcc tgttcaacga 840
174 accgcgccag gccaaaggcg cttcggaccg cttcgccaag gccggcccgg acgtgcagcc 900
175 gtgtcgccca acggcctgct gcagttcccc tcccgcgcg gcgcagctg gcatgtcggc 960
176 ggcgcccaca ccaacaccgg ctccgggcaat taccgatgt cgtcgtgga catgtcgcgc 1020
177 ggcggcggtt ggggcagcaa ccagaacggc aactgggtgt cggcctcggc cgcgggtcg 1080
178 ttcaagcgcc actcttcgtg cttcgcggag atcgtgcaca ccggcggtg gtcgacgacc 1140
179 tactaccacc tgatgaacat ccagtacaac accggcgcca acgtgtcgat gaacaccgcc 1200
180 atcgccaacc cggccaacac ccaggcgagc gcgtgtgca acggcggcca gtcgaccggc 1260
181 ccgcacgagc attggtcggt gaagcagaac ggcagcttct accacctcaa cggcacctac 1320
182 ctgtcggggt atcgcatcac cgcgaccggc agcagctatg acaccaactg cagccgggtc 1380
183 tatctgacca agaaccggca gaactactgc tacggctatt acgtcaacct gggcccgaac 1440

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184 tgaggctcgc cgcgtgcgtt gcccgcgctcc tcaagcgccc cgcgcgcggg gcgcgggcac 1500
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188 <210> SEQ ID NO: 5
189 <211> LENGTH: 480
190 <212> TYPE: PRT
191 <213> ORGANISM: Staphylococcus simulans
193 <400> SEQUENCE: 5
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198           20           25           30
200 Glu Thr His Ala Ser Glu Lys Ser Asn Met Asp Val Ser Lys Lys Val
201           35           40           45
203 Ala Glu Val Glu Thr Ser Lys Pro Pro Val Glu Asn Thr Ala Glu Val
204           50           55           60
206 Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser
207   65           70           75           80
209 Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro
210           85           90           95
212 Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn
213           100          105          110
215 Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu
216           115          120          125
218 Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr
219           130          135          140
221 Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala
222  145          150          155          160
224 Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu
225           165          170          175
227 Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala
228           180          185          190
230 Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu
231           195          200          205
233 Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys
234           210          215          220
236 Ala Leu Val Gln Asn Arg Thr Ala Leu Arg Ala Ala Thr His Glu His
237  225          230          235          240
239 Ser Ala Gln Trp Leu Asn Asn Tyr Lys Tyr Gly Tyr Gly Tyr Gly Pro
240           245          250          255
242 Tyr Pro Leu Gly Ile Asn Gly Gly Ile His Tyr Gly Val Asp Phe Phe
243           260          265          270
245 Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val
246           275          280          285
248 Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile
249           290          295          300
251 Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser Lys Tyr
252  305          310          315          320
254 Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp
255           325          330          335

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257 Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe Gln Arg
258           340           345           350
260 Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe
261           355           360           365
263 Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr
264           370           375           380
266 Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser
267 385           390           395           400
269 Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr
270           405           410           415
272 Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln
273           420           425           430
275 Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val
276           435           440           445
278 Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr
279           450           455           460
281 Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
282 465           470           475           480
288 <210> SEQ ID NO: 6
289 <211> LENGTH: 492
290 <212> TYPE: PRT
291 <213> ORGANISM: Achromobacter lyticus
293 <400> SEQUENCE: 6
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298           20           25           30
300 Glu Thr His Ala Ser Glu Lys Ser Asn Met Asp Val Ser Lys Lys Val
301           35           40           45
303 Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val
304           50           55           60
306 Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser
307 65           70           75           80
309 Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro
310           85           90           95
312 Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn
313           100          105          110
315 Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu
316           115          120          125
318 Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr
319           130          135          140
321 Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala
322 145          150          155          160
324 Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu
325           165          170          175
327 Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala
328           180          185          190
330 Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu
331           195          200          205

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VERIFICATION SUMMARY

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